

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Burkly, Linda C.
- (ii) TITLE OF INVENTION: Treatment for Insulin Dependent Diabetes
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Allegretti & Witcoff, Ltd.
 - (B) STREET: 10 South Wacker Drive, Suite 3000
 - (C) CITY: Chicago
 - (D) STATE: IL
 - (E) COUNTRY: US
 - (F) ZIP: 60606
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 9 February 1993
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: McNicholas, Janet M.
 - (B) REGISTRATION NUMBER: 32,918
 - (C) REFERENCE/DOCKET NUMBER: 92,749; D015 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312-715-1000
 - (B) TELEFAX: 312-715-1234

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1

(D) OTHER INFORMATION: /note= "pBAG159 insert: HP1/2 heavy chain variable region; amino acid 1 is Glu (E) but Gln (Q) may be substituted"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTC AAA CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG CCA GGG GCC TCA	48
Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser	
2 6 11 16	
GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT AAA GAC ACC TAT	96
Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr	
21 26 31	
ATG CAC TGG GTG AAG CAG AGG CCT GAA CAG GGC CTG GAG TGG ATT GGA	144
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly	
36 41 46	
AGG ATT GAT CCT GCG AGT GGC GAT ACT AAA TAT GAC CCG AAG TTC CAG	192
Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln	
51 56 61	
GTC AAG GCC ACT ATT ACA GCG GAC ACG TCC TCC AAC ACA GCC TGG CTG	240
Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu	
66 71 76 81	
CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC TAC TAC TGT GCA	288
Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala	
86 91 96	
GAC GGA ATG TGG GTA TCA ACG GGA TAT GCT CTG GAC TTC TGG GGC CAA	336
Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln	
101 106 111	
GGG ACC ACG GTC ACC GTC TCC TCA	360
Gly Thr Thr Val Thr Val Ser Ser	
116 121	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Val Lys Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala Ser
2 6 11 16

Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr
21 26 31

Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly
36 41 46

Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp Pro Lys Phe Gln
51 56 61

Val Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Trp Leu
66 71 76 81

Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
86 91 96

Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp Phe Trp Gly Gln
101 106 111

Gly Thr Thr Val Thr Val Ser Ser
116 121

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..318
- (D) OTHER INFORMATION: /product= "HP1/2 light chain
variable region"

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light
chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AGT	ATT	GTG	ATG	ACC	CAG	ACT	CCC	AAA	TTC	CTG	CTT	GTT	TCA	GCA	GGA	48
Ser	Ile	Val	Met	Thr	Gln	Thr	Pro	Lys	Phe	Leu	Leu	Val	Ser	Ala	Gly	
1				5					10					15		
GAC	AGG	GTT	ACC	ATA	ACC	TGC	AAG	GCC	AGT	CAG	AGT	GTG	ACT	AAT	GAT	96
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Thr	Asn	Asp	
			20					25					30			
GTA	GCT	TGG	TAC	CAA	CAG	AAG	CCA	GGG	CAG	TCT	CCT	AAA	CTG	CTG	ATA	144
Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	
		35					40					45				
TAT	TAT	GCA	TCC	AAT	CGC	TAC	ACT	GGA	GTC	CCT	GAT	CGC	TTC	ACT	GGC	192
Tyr	Tyr	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	
	50					55					60					
AGT	GGA	TAT	GGG	ACG	GAT	TTC	ACT	TTC	ACC	ATC	AGC	ACT	GTG	CAG	GCT	240
Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Thr	Val	Gln	Ala	
65					70					75					80	
GAA	GAC	CTG	GCA	GTT	TAT	TTC	TGT	CAG	CAG	GAT	TAT	AGC	TCT	CCG	TAC	288
Glu	Asp	Leu	Ala	Val	Tyr	Phe	Cys	Gln	Gln	Asp	Tyr	Ser	Ser	Pro	Tyr	
				85				90						95		
ACG	TTC	GGA	GGG	GGG	ACC	AAG	CTG	GAG	ATC							318
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile							
			100				105									

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ser	Ile	Val	Met	Thr	Gln	Thr	Pro	Lys	Phe	Leu	Leu	Val	Ser	Ala	Gly
1				5					10					15	
Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	Thr	Asn	Asp
			20					25					30		
Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile
		35				40						45			

Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val Pro Asp Arg Phe Thr Gly
50 55 60

Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr Ile Ser Thr Val Gln Ala
65 70 75 80

Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln Asp Tyr Ser Ser Pro Tyr
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
100 105

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..57

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 58..429

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..429

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "pBAG195 insert: AS heavy chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GAC TGG ACC TGG AGG GTC TTC TGC TTG CTG GCT GTA GCA CCA GGT	48
Met Asp Trp Thr Trp Arg Val Phe Cys Leu Leu Ala Val Ala Pro Gly	
-19 -15 -10 -5	
GCC CAC TCC CAG GTC CAA CTG CAG GAG AGC GGT CCA GGT CTT GTG AGA	96
Ala His Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Arg	
1 5 10	

CCT	AGC	CAG	ACC	CTG	AGC	CTG	ACC	TGC	ACC	GCG	TCT	GGC	TTC	AAC	ATT	144
Pro	Ser	Gln	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile	
	15					20					25					
AAA	GAC	ACC	TAT	ATG	CAC	TGG	GTG	AGA	CAG	CCA	CCT	GGA	CGA	GGT	CTT	192
Lys	Asp	Thr	Tyr	Met	His	Trp	Val	Arg	Gln	Pro	Pro	Gly	Arg	Gly	Leu	
	30				35					40					45	
GAG	TGG	ATT	GGA	AGG	ATT	GAT	CCT	GCG	AGT	GGC	GAT	ACT	AAA	TAT	GAC	240
Glu	Trp	Ile	Gly	Arg	Ile	Asp	Pro	Ala	Ser	Gly	Asp	Thr	Lys	Tyr	Asp	
				50					55					60		
CCG	AAG	TTC	CAG	GTC	AGA	GTG	ACA	ATG	CTG	GTA	GAC	ACC	AGC	AGC	AAC	288
Pro	Lys	Phe	Gln	Val	Arg	Val	Thr	Met	Leu	Val	Asp	Thr	Ser	Ser	Asn	
			65					70					75			
CAG	TTC	AGC	CTG	AGA	CTC	AGC	AGC	GTG	ACA	GCC	GCC	GAC	ACC	GCG	GTC	336
Gln	Phe	Ser	Leu	Arg	Leu	Ser	Ser	Val	Thr	Ala	Ala	Asp	Thr	Ala	Val	
		80				85						90				
TAT	TAT	TGT	GCA	GAC	GGA	ATG	TGG	GTA	TCA	ACG	GGA	TAT	GCT	CTG	GAC	384
Tyr	Tyr	Cys	Ala	Asp	Gly	Met	Trp	Val	Ser	Thr	Gly	Tyr	Ala	Leu	Asp	
	95					100					105					
TTC	TGG	GGC	CAA	GGG	ACC	ACG	GTC	ACC	GTC	TCC	TCA	GGT	GAG	TCC		429
Phe	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Glu	Ser		
110					115					120						

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asp	Trp	Thr	Trp	Arg	Val	Phe	Cys	Leu	Leu	Ala	Val	Ala	Pro	Gly
-19				-15					-10					-5	
Ala	His	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ser	Gly	Pro	Gly	Leu	Val	Arg
			1				5					10			
Pro	Ser	Gln	Thr	Leu	Ser	Leu	Thr	Cys	Thr	Ala	Ser	Gly	Phe	Asn	Ile
	15					20					25				
Lys	Asp	Thr	Tyr	Met	His	Trp	Val	Arg	Gln	Pro	Pro	Gly	Arg	Gly	Leu
30					35					40					45

Glu Trp Ile Gly Arg Ile Asp Pro Ala Ser Gly Asp Thr Lys Tyr Asp
50 55 60

Pro Lys Phe Gln Val Arg Val Thr Met Leu Val Asp Thr Ser Ser Asn
65 70 75

Gln Phe Ser Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val
80 85 90

Tyr Tyr Cys Ala Asp Gly Met Trp Val Ser Thr Gly Tyr Ala Leu Asp
95 100 105

Phe Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Glu Ser
110 115 120

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
- (B) LOCATION: 1..57

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 58..386

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..386

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /note= "pBAG198 insert: VK2 (SVMDY)
light chain variable region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GGT TGG TCC TGC ATC ATC CTG TTC CTG GTT GCT ACC GCT ACC GGT
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

GTC	CAC	TCC	AGC	ATC	GTG	ATG	ACC	CAG	AGC	CCA	AGC	AGC	CTG	AGC	GCC	96
Val	His	Ser	Ser	Ile	Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	
			1				5					10				
AGC	GTG	GGT	GAC	AGA	GTG	ACC	ATC	ACC	TGT	AAG	GCC	AGT	CAG	AGT	GTG	144
Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val	
	15					20					25					
ACT	AAT	GAT	GTA	GCT	TGG	TAC	CAG	CAG	AAG	CCA	GGT	AAG	GCT	CCA	AAG	192
Thr	Asn	Asp	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	
	30				35				40						45	
CTG	CTG	ATC	TAC	TAT	GCA	TCC	AAT	CGC	TAC	ACT	GGT	GTG	CCA	GAT	AGA	240
Leu	Leu	Ile	Tyr	Tyr	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg	
			50					55					60			
TTC	AGC	GGT	AGC	GGT	TAT	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC	288
Phe	Ser	Gly	Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	
			65				70						75			
CTC	CAG	CCA	GAG	GAC	ATC	GCC	ACC	TAC	TAC	TGC	CAG	CAG	GAT	TAT	AGC	336
Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Asp	Tyr	Ser	
		80				85						90				
TCT	CCG	TAC	ACG	TTC	GGC	CAA	GGG	ACC	AAG	GTG	GAA	ATC	AAA	CGT	AAG	TG
Ser	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Lys	
	95				100					105						

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly
-19				-15			-10							-5	
Val	His	Ser	Ser	Ile	Val	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala
			1				5					10			
Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Ser	Val
	15					20					25				
Thr	Asn	Asp	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys
30					35					40					45

Leu	Leu	Ile	Tyr	Tyr	Ala	Ser	Asn	Arg	Tyr	Thr	Gly	Val	Pro	Asp	Arg
				50					55					60	
Phe	Ser	Gly	Ser	Gly	Tyr	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser
			65					70					75		
Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Asp	Tyr	Ser
		80					85					90			
Ser	Pro	Tyr	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg	Lys
	95					100					105				